

## SEQUENCE LISTING

<110> Serizawa, Nobufusa  
 Haruyama, Hideyuki  
 Nakahara, Kaori  
 Tamaki, Ikuko  
 Takahashi, Tohru

<120> Anti-Fas Antibodies

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 US 09/408,646  
 JP 9-82953  
 JP 9-169088  
 JP 9-276064  
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Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys	
-1 1 5 10	
cct ggg gct tca gtg aag ctg tcc tgc aag gct tct ggc tac acc ttc	144
Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
15 20 25	
acc agc tac tgg atg cag tgg gta aaa cag agg cct gga cag ggc ctt	192
Thr Ser Tyr Trp Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu	
30 35 40 45	
gag tgg atc gga gag att gat cct tct gat agc tat act aac tac aat	240
Glu Trp Ile Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn	
50 55 60	
caa aag ttc aag ggc aag gcc aca ttg act gta gac aca tcc tcc agc	288
Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser	
65 70 75	
aca gcc tac atg cag ctc agc agc ctg aca tct gag gac tct gcg gtc	336
Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val	
80 85 90	
tat tac tgt gca aga aat agg gac tat agt aac aac tgg tac ttc gat	384
Tyr Tyr Cys Ala Arg Asn Arg Asp Tyr Ser Asn Asn Trp Tyr Phe Asp	
95 100 105	
gtc tgg ggc aca ggg acc acg gtc acc gtc tcc tca gcc aaa acg aca	432
Val Trp Gly Thr Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr	
110 115 120 125	
ccc cca tct gtc tat cca ctg gcc cct gga tct gct gcc caa act aac	480
Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn	
130 135 140	
tcc atg gtg acc ctg gga tgc ctg gtc aag ggc tat ttc cct gag cca	528
Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro	
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gtg aca gtg acc tgg aac tct gga tcc ctg tcc agc ggt gtg cac acc	576
Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr	
160 165 170	
ttc cca gct gtc ctg cag tct gac ctc tac act ctg agc agc tca gtg	624

Phe	Pro	Ala	Val	Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	Ser	Val	
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act	gtc	ccc	tcc	agc	acc	tgg	ccc	agc	cag	acc	gtc	acc	tgc	aac	gtt	672
Thr	Val	Pro	Ser	Ser	Thr	Trp	Pro	Ser	Gln	Thr	Val	Thr	Cys	Asn	Val	
190					195					200					205	
gcc	cac	ccg	gcc	agc	agc	acc	aag	gtg	gac	aag	aaa	att	gtg	ccc	agg	720
Ala	His	Pro	Ala	Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val	Pro	Arg	
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gat	tgt	ggt	tgt	aag	cct	tgc	ata	tgt	aca	gtc	cca	gaa	gta	tca	tct	768
Asp	Cys	Gly	Cys	Lys	Pro	Cys	Ile	Cys	Thr	Val	Pro	Glu	Val	Ser	Ser	
			225					230					235			
gtc	ttc	atc	ttc	ccc	cca	aag	ccc	aag	gat	gtg	ctc	acc	att	act	ctg	816
Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr	Ile	Thr	Leu	
		240					245					250				
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Thr	Pro	Lys	Val	Thr	Cys	Val	Val	Val	Asp	Ile	Ser	Lys	Asp	Asp	Pro	
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Glu	Val	Gln	Phe	Ser	Trp	Phe	Val	Asp	Asp	Val	Glu	Val	His	Thr	Ala	
270					275					280					285	
cag	acg	caa	ccc	cgg	gag	gag	cag	ttc	aac	agc	act	ttc	cgc	tca	gtc	960
Gln	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe	Arg	Ser	Val	
				290					295					300		
agt	gaa	ctt	ccc	atc	atg	cac	cag	aac	tgg	ctc	aat	ggc	aag	gag	ttc	1008
Ser	Glu	Leu	Pro	Ile	Met	His	Gln	Asn	Trp	Leu	Asn	Gly	Lys	Glu	Phe	
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aaa	tgc	agg	gtc	aac	agt	gca	gct	ttc	cct	gcc	ccc	atc	gag	aaa	acc	1056
Lys	Cys	Arg	Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala	Pro	Ile	Glu	Lys	Thr	
		320					325					330				
atc	tcc	aaa	acc	aaa	ggc	aga	ccg	aag	gct	cca	cag	gtg	tac	acc	att	1104
Ile	Ser	Lys	Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro	Gln	Val	Tyr	Thr	Ile	
	335					340					345					
cca	cct	ccc	aag	gag	cag	atg	gcc	aag	gat	aaa	gtc	agt	ctg	acc	tgc	1152
Pro	Pro	Pro	Lys	Glu	Gln	Met	Ala	Lys	Asp	Lys	Val	Ser	Leu	Thr	Cys	
350					355					360					365	
atg	ata	aca	gac	ttc	ttc	cct	gaa	gac	att	act	gtg	gag	tgg	cag	tgg	1200
Met	Ile	Thr	Asp	Phe	Phe	Pro	Glu	Asp	Ile	Thr	Val	Glu	Trp	Gln	Trp	
				370					375					380		

aat ggg cag cca gcg gag aac tac aag aac act cag ccc atc atg aac 1248  
 Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asn  
                   385                                  390                                  395

acg aat ggc tct tac ttc gtc tac agc aag ctc aat gtg cag aag agc 1296  
 Thr Asn Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser  
                   400                                  405                                  410

aac tgg gag gca gga aat act ttc acc tgc tct gtg tta cat gag ggc 1344  
 Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly  
                   415                                  420                                  425

ctg cac aac cac cat act gag aag agc ctc tcc cac tct cct ggt aaa 1392  
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Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
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Thr Ser Tyr Trp Met Gln Trp Val Lys Gln Arg Pro Gly Gln Gly Leu  
                   30                                  35                                  40                                  45

Glu Trp Ile Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn  
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Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Ser Ser  
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Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val  
                   80                                  85                                  90

Tyr Tyr Cys Ala Arg Asn Arg Asp Tyr Ser Asn Asn Trp Tyr Phe Asp  
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Val Trp Gly Thr Gly Thr Thr Val Thr Val Ser Ser Ala Lys Thr Thr  
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Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn  
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Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro  
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 Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr  
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 Thr Val Pro Ser Ser Thr Trp Pro Ser Gln Thr Val Thr Cys Asn Val  
 190 195 200 205  
 Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val Pro Arg  
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 Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val Ser Ser  
 225 230 235  
 Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile Thr Leu  
 240 245 250  
 Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp Asp Pro  
 255 260 265  
 Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His Thr Ala  
 270 275 280 285  
 Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val  
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 Ser Glu Leu Pro Ile Met His Gln Asn Trp Leu Asn Gly Lys Glu Phe  
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 Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr  
 320 325 330  
 Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile  
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 Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys  
 350 355 360 365  
 Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp  
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 385 390 395  
 Thr Asn Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser  
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 ggc tcc act ggt gac att gtg ctg acc caa tct cca gct tct ttg gct 96  
 Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala  
 -1 1 5 10  
 gtg tct cta ggg cag agg gcc acc atc tcc tgc aag gcc agc caa agt 144  
 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser  
 15 20 25  
 gtt gat tat gat ggt gat agt tat atg aac tgg tac caa cag aaa cca 192  
 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro  
 30 35 40  
 gga cag cca ccc aaa ctc ctc atc tat gct gca tcc aat cta gaa tct 240  
 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser  
 45 50 55 60  
 ggg atc cca gcc agg ttt agt ggc agt ggg tct ggg aca gac ttc acc 288  
 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
 65 70 75  
 ctc aac atc cat cct gtg gag gag gag gat gct gca acc tat tac tgt 336  
 Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys  
 80 85 90  
 cag caa agt aat gag gat cct cgg acg ttc ggt gga ggc acc aag ctg 384  
 Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu  
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Glu	Ile	Lys	Arg	Ala	Asp	Ala	Ala	Pro	Thr	Val	Ser	Ile	Phe	Pro	Pro	
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Ser	Ser	Glu	Gln	Leu	Thr	Ser	Gly	Gly	Ala	Ser	Val	Val	Cys	Phe	Leu	
125					130					135					140	
aac	aac	ttc	tac	ccc	aaa	gac	atc	aat	gtc	aag	tgg	aag	att	gat	ggc	528
Asn	Asn	Phe	Tyr	Pro	Lys	Asp	Ile	Asn	Val	Lys	Trp	Lys	Ile	Asp	Gly	
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agt	gaa	cga	caa	aat	ggc	gtc	ctg	aac	agt	tgg	act	gat	cag	gac	agc	576
Ser	Glu	Arg	Gln	Asn	Gly	Val	Leu	Asn	Ser	Trp	Thr	Asp	Gln	Asp	Ser	
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aaa	gac	agc	acc	tac	agc	atg	agc	agc	acc	ctc	acg	ttg	acc	aag	gac	624
Lys	Asp	Ser	Thr	Tyr	Ser	Met	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Lys	Asp	
			175				180					185				
gag	tat	gaa	cga	cat	aac	agc	tat	acc	tgt	gag	gcc	act	cac	aag	aca	672
Glu	Tyr	Glu	Arg	His	Asn	Ser	Tyr	Thr	Cys	Glu	Ala	Thr	His	Lys	Thr	
	190					195					200					
tca	act	tca	ccc	att	gtc	aag	agc	ttc	aac	agg	aat	gag	tgt			714
Ser	Thr	Ser	Pro	Ile	Val	Lys	Ser	Phe	Asn	Arg	Asn	Glu	Cys			
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 -1 1 5 10  
 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser  
 15 20 25  
 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro  
 30 35 40  
 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser  
 45 50 55 60  
 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
 65 70 75



Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys  
                             80                            85                            90  
 Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu  
                             95                            100                            105  
 Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro  
             110                            115                            120  
 Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu  
 125                            130                            135                            140  
 Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly  
                             145                            150                            155  
 Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser  
                             160                            165                            170  
 Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp  
                             175                            180                            185  
 Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr  
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<210> 12  
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<220>  
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         human Fas antigen

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34

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<220>  
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         human Fas antigen

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<220>  
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35

<210> 15  
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 <212> DNA  
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<220>  
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<210> 17  
 <211> 22  
 <212> PRT  
 <213> Mus musculus

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Gln Arg Ala Thr Ile Ser  
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chain gamma 1 subtype 2b

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19

<210> 19  
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chain gamma 1 subtype 2b

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<210> 20  
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<212> DNA  
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20

<210> 21  
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## chain kappa subtype 3

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 anti-human Fas antibody HFE7A

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 anti-human Fas antibody HFE7A

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<210> 24  
 <211> 29  
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 to subclone a cDNA encoding the light chain of  
 anti-human Fas antibody HFE7A

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<210> 25  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Adaptor primer  
to subclone a cDNA encoding the light chain of  
anti-human Fas antibody HFE7A

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37

<210> 26

<211> 19

<212> PRT

<213> Homo sapiens

<400> 26

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Lys Gly Leu

<210> 27

<211> 19

<212> PRT

<213> Homo sapiens

<400> 27

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1				5					10					15	

Thr Val Glu

<210> 28

<211> 20

<212> PRT

<213> Homo sapiens

<400> 28

Glu	Leu	Arg	Lys	Thr	Val	Thr	Thr	Val	Glu	Thr	Gln	Asn	Leu	Glu	Gly
1				5					10					15	

Leu	His	His	Asp
			20

<210> 29

<211> 20

<212> PRT

<213> Homo sapiens

<400> 29

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Pro Cys Pro Pro  
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<210> 30  
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 1 5 10 15

Asp Cys Thr Val  
 20

<210> 31  
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 <213> Homo sapiens

<400> 31  
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 1 5 10 15

Cys Val Pro Cys Gln  
 20

<210> 32  
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 <213> Homo sapiens

<400> 32  
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Thr Asp Lys Ala  
 20

<210> 33  
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<400> 33  
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Arg Cys Arg

<210> 34  
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Gly Leu Glu Val  
                     20

<210> 35  
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     1                    5                    10                    15

Thr Gln Asn Thr  
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 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg Cys Lys Pro  
     1                    5                    10                    15

Asn Phe Phe Cys  
                     20

<210> 37  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 37  
 Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu  
     1                    5                    10                    15

His Cys Asp Pro  
                     20

<210> 38  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 38  
 Asn Ser Thr Val Cys Glu His Cys Asp Pro Cys Thr Lys Cys Glu His  
     1                    5                    10                    15

Gly Ile Ile Lys  
                     20

<210> 39  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 39  
 Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr Ser  
     1                    5                    10                    15

Asn Thr Lys Cys  
                     20

<210> 40  
 <211> 18  
 <212> PRT  
 <213> Homo sapiens

<400> 40  
 Glu Cys Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg  
     1                    5                    10                    15

Ser Asn

<210> 41  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 41  
 Ser Ser Gly Lys Tyr Glu Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala  
     1                    5                    10                    15

Phe Asn Val Glu  
                     20

<210> 42



<211> 10  
 <212> PRT  
 <213> Homo sapiens

<400> 42  
 His Gly Leu Glu Val Glu Ile Asn Cys Thr  
           1                          5                          10

<210> 43  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<400> 43  
 Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr  
           1                          5                          10

<210> 44  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
 Lys Cys Arg Cys Lys Pro Asn Phe Phe Cys  
           1                          5                          10

<210> 45  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
 Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp  
           1                          5                          10

<210> 46  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Gly Lys Ile Ala Ser Cys Leu Asn Asp Asn  
           1                          5                          10

<210> 47  
 <211> 34  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
gcgaattctg ccttgactga tcagagtttc ctca

34

<210> 48  
<211> 32  
<212> DNA  
<213> Homo sapiens

<400> 48  
gctctagatg aggtgaaaga tgagctggag ga

32

<210> 49  
<211> 768  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> CDS  
<222> (40)..(753)

<220>  
<221> mat peptide  
<222> (100)..(753)

<220>  
<221> sig peptide  
<222> (40)..(99)

<220>  
<223> Description of Artificial Sequence: Designed DNA  
encoding the light chain of humanized anti-human  
Fas antibody

<400> 49  
cccaagctta agaagcatcc tctcatctag ttctcagag atg gag aca gac aca  
Met Glu Thr Asp Thr  
-20

54

atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca ggc tcc act ggt gac  
Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser Thr Gly Asp  
-15 -10 -5 -1 1

102

att gtg ctc acc caa tct cca ggt act ttg tct ctg tct cca ggg gag  
Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu  
5 10 15

150

agg gcc acc ctc tcc tgc aag gcc agc caa agt gtt gat tat gat ggt  
Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly  
20 25 30

198

gat	agt	tat	atg	aac	tgg	tac	caa	cag	aaa	cca	gga	cag	gca	ccc	aga	246
Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	
	35					40					45					
ctc	ctc	atc	tat	gct	gca	tcc	aat	ctc	gaa	tct	ggg	atc	cca	gac	agg	294
Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Asp	Arg	
	50				55					60					65	
ttt	agt	ggc	agt	ggg	tct	ggg	aca	gac	ttc	acc	ctc	acc	atc	tct	cgt	342
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	
				70					75					80		
ctg	gag	ccg	gcg	gat	ttt	gca	gtc	tat	tac	tgt	cag	caa	agt	aat	gag	390
Leu	Glu	Pro	Ala	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn	Glu	
			85					90					95			
gat	cct	cgg	acg	ttc	ggg	caa	ggc	acc	agg	ctg	gaa	atc	aaa	cgg	act	438
Asp	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys	Arg	Thr	
		100					105					110				
gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	cag	ttg	486
Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	
	115					120					125					
aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	ttc	tat	ccc	534
Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	
	130				135					140					145	
aga	gag	gcc	aaa	gta	cag	tgg	aaa	gtg	gat	aac	gcc	ctc	caa	tcg	ggg	582
Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	
				150					155					160		
aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	agc	aag	gac	agc	acc	tac	630
Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	
			165					170					175			
agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	gca	gac	tac	gag	aaa	cac	678
Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	
		180					185					190				
aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	ggc	ctg	agc	tcg	ccc	gtc	726
Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	
	195					200					205					
aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tagtaagaat	tcggg						768
Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys								
	210				215											

<210> 50  
 <211> 238  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Designed light chain of humanized anti-Fas antibody

&lt;400&gt; 50

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 -20 -15 -10 -5

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser  
 -1 1 5 10

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser  
 15 20 25

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro  
 30 35 40

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser  
 45 50 55 60

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
 65 70 75

Leu Thr Ile Ser Arg Leu Glu Pro Ala Asp Phe Ala Val Tyr Tyr Cys  
 80 85 90

Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Arg Leu  
 95 100 105

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
 110 115 120

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
 125 130 135 140

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
 145 150 155

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
 160 165 170

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala  
 175 180 185

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
 190 195 200

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 205 210 215

&lt;210&gt; 51

&lt;211&gt; 768

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (40)..(753)

&lt;220&gt;

&lt;221&gt; mat peptide

&lt;222&gt; (100)..(753)

&lt;220&gt;

&lt;221&gt; sig peptide

&lt;222&gt; (40)..(99)

&lt;220&gt;

<223> Description of Artificial Sequence: Designed DNA  
encoding the light chain of humanized anti-human  
Fas antibody

&lt;400&gt; 51

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cccaagctta agaagcatcc tctcatctag ttctcagag atg gag aca gac aca      54
                                   Met Glu Thr Asp Thr
                                   -20

atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca ggc tcc act ggt gac      102
Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser Thr Gly Asp
-15                               -10                               -5                               -1    1

att gtg ctc acc caa tct cca ggt act ttg tct ctg tct cca ggg gag      150
Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu
                    5                               10                               15

agg gcc acc ctc tcc tgc aag gcc agc caa agt gtt gat tat gat ggt      198
Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly
                20                               25                               30

gat agt tat atg aac tgg tac caa cag aaa cca gga cag gca ccc aga      246
Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg
        35                               40                               45

ctc ctc atc tat gct gca tcc aat ctc gaa tct ggg atc cca gac agg      294
Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Ile Pro Asp Arg
        50                               55                               60                               65

ttt agt ggc agt ggg tct ggg aca gac ttc acc ctc acc atc cat cct      342
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile His Pro
                                70                               75                               80

gtg gag gag gag gat gct gca acc tat tac tgt cag caa agt aat gag      390
Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
                        85                               90                               95

```

gat	cct	cgg	acg	ttc	ggg	caa	ggc	acc	agg	ctg	gaa	atc	aaa	cgg	act	438
Asp	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys	Arg	Thr	
	100						105					110				
gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	cag	ttg	486
Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	
	115					120					125					
aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	ttc	tat	ccc	534
Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	
130					135					140					145	
aga	gag	gcc	aaa	gta	cag	tgg	aaa	gtg	gat	aac	gcc	ctc	caa	tcg	ggg	582
Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	
				150					155					160		
aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	agc	aag	gac	agc	acc	tac	630
Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	
		165						170					175			
agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	gca	gac	tac	gag	aaa	cac	678
Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	
		180				185						190				
aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	ggc	ctg	agc	tcg	ccc	gtc	726
Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	
	195					200					205					
aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tagtaagaat	tcggg						768
Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys								
210					215											

<210> 52  
 <211> 238  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Designed light chain of humanized anti-Fas antibody

<400> 52  
 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 -20 -15 -10 -5  
 Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser  
 -1 1 5 10  
 Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser  
 15 20 25  
 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro  
 30 35 40

Gly Gln Ala Pro Arg Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser  
 45 50 55 60  
 Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
 65 70 75  
 Leu Thr Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys  
 80 85 90  
 Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Arg Leu  
 95 100 105  
 Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
 110 115 120  
 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
 125 130 135 140  
 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
 145 150 155  
 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
 160 165 170  
 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala  
 175 180 185  
 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
 190 195 200  
 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 205 210 215

<210> 53  
 <211> 768  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (40)..(753)

<220>  
 <221> mat peptide  
 <222> (100)..(753)

<220>  
 <221> sig peptide  
 <222> (40)..(99)

<220>  
 <223> Description of Artificial Sequence: Designed DNA  
 encoding the light chain of humanized anti-human

## Fas antibody

&lt;400&gt; 53

cccaagctta	agaagcatcc	tctcatctag	ttctcagag	atg	gag	aca	gac	aca	54							
				Met	Glu	Thr	Asp	Thr								
				-20												
atc	ctg	cta	tgg	gtg	ctg	ctg	ctc	tgg	gtt	cca	ggc	tcc	act	ggt	gac	102
Ile	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro	Gly	Ser	Thr	Gly	Asp	
-15					-10					-5				-1	1	
att	gtg	ctc	acc	caa	tct	cca	ggg	act	ttg	tct	ctg	tct	cca	ggg	gag	150
Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	
			5					10					15			
agg	gcc	acc	ctc	tcc	tgc	aag	gcc	agc	caa	agt	gtt	gat	tat	gat	ggt	198
Arg	Ala	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp	Gly	
		20					25					30				
gat	agt	tat	atg	aac	tgg	tac	caa	cag	aaa	cca	gga	cag	cca	ccc	aaa	246
Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	
	35					40					45					
ctc	ctc	atc	tat	gct	gca	tcc	aat	ctc	gaa	tct	ggg	atc	cca	gac	agg	294
Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Asp	Arg	
50					55					60					65	
ttt	agt	ggc	agt	ggg	tct	ggg	aca	gac	ttc	acc	ctc	acc	atc	cat	cct	342
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	His	Pro	
				70					75					80		
gtg	gag	gag	gag	gat	gct	gca	acc	tat	tac	tgt	cag	caa	agt	aat	gag	390
Val	Glu	Glu	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn	Glu	
			85					90					95			
gat	cct	cgg	acg	ttc	ggg	caa	ggc	acc	agg	ctg	gaa	atc	aaa	cgg	act	438
Asp	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Arg	Leu	Glu	Ile	Lys	Arg	Thr	
		100					105					110				
gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	cag	ttg	486
Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	
	115					120					125					
aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	ttc	tat	ccc	534
Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	
130					135					140					145	
aga	gag	gcc	aaa	gta	cag	tgg	aaa	gtg	gat	aac	gcc	ctc	caa	tcg	ggt	582
Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	
				150					155					160		
aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	agc	aag	gac	agc	acc	tac	630
Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	
			165					170					175			



agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac 678  
 Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His  
           180                                  185                                  190

aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc 726  
 Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val  
           195                                  200                                  205

aca aag agc ttc aac agg gga gag tgt tagtaagaat tcggg 768  
 Thr Lys Ser Phe Asn Arg Gly Glu Cys  
           210                                  215

<210> 54

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed light  
 chain of humanized anti-Fas antibody

<400> 54

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 -20                                  -15                                  -10                                  -5

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser  
                   -1      1                                  5                                  10

Leu Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Lys Ala Ser Gln Ser  
           15                                  20                                  25

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro  
           30                                  35                                  40

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser  
           45                                  50                                  55                                  60

Gly Ile Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
                   65                                  70                                  75

Leu Thr Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys  
                   80                                  85                                  90

Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Arg Leu  
           95                                  100                                  105

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
           110                                  115                                  120

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
           125                                  130                                  135                                  140

<220>  
<223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of humanized anti-Fas antibody

<400> 57  
ccaggtactt tgtctctgtc tccaggggag agggccaccc tctc

44

<210> 58  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the light  
chain of humanized anti-Fas antibody

<400> 58  
gattcgagat tggatgcagc atagatgagg agtctgggtg cctg

44

<210> 59  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the light  
chain of humanized anti-Fas antibody

<400> 59  
gctgcatcca atctcgaatc tgggatccca gacagggtta gtggc

45

<210> 60  
<211> 52  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the light  
chain of humanized anti-Fas antibody

<400> 60  
aaaatccgcc ggctccagac gagagatggt gaggggtgaag tctgtcccag ac

52

<210> 61  
<211> 58  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the light

## chain of humanized anti-Fas antibody

<400> 61  
ctcgtctgga gccggcggat ttgcagtct attactgtca gcaaagtaat gaggatcc 58

<210> 62  
<211> 55  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the light  
chain of humanized anti-Fas antibody

<400> 62  
tgaagacaga tggcgcagcc acagtcggtt tgatttccag cctggcgcct tgacc 55

<210> 63  
<211> 55  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the light  
chain of humanized anti-Fas antibody

<400> 63  
ggtcaaggca ccaggctgga aatcaaacgg actgtggctg caccatctgt cttca 55

<210> 64  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the light  
chain of humanized anti-Fas antibody

<400> 64  
cccgaattct tactaacact ctcccctggt gaagctcttt gtgac 45

<210> 65  
<211> 55  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of humanized anti-Fas antibody

<400> 65

tctgtcccag acccactgcc actaaacctg tctgggatcc cagattcgag attgg

55

<210> 66

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of humanized anti-Fas antibody

<400> 66

gtttagtggc agtgggtctg ggacagactt cacctctacc atccatcctg tggag

55

<210> 67

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of humanized anti-Fas antibody

<400> 67

atggtgcagc cacagtccgt ttgatttcca gcctggtgcc ttgaccgaac gtccg

55

<210> 68

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sequencing primer for DNAs encoding the light chains of humanized anti-Fas antibodies

<400> 68

cccaagctta agaagcatcc

20

<210> 69

<211> 20

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Sequencing  
primer for DNAs encoding the light chains of  
humanized anti-Fas antibodies

&lt;400&gt; 69

atctatgctg catccaatct

20

&lt;210&gt; 70

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Sequencing  
primer for DNAs encoding the light chains of  
humanized anti-Fas antibodies

&lt;400&gt; 70

gttgtgtgcc tgctgaataa

20

&lt;210&gt; 71

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Sequencing  
primer for DNAs encoding the light chains of  
humanized anti-Fas antibodies

&lt;400&gt; 71

cccgaattct tactaacact

20

&lt;210&gt; 72

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Sequencing  
primer for DNAs encoding the light chains of  
humanized anti-Fas antibodies

&lt;400&gt; 72

ttattcagca ggcacacaac

20

&lt;210&gt; 73

&lt;211&gt; 20

&lt;212&gt; DNA

## &lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Sequencing  
primer for DNAs encoding the light chains of  
humanized anti-Fas antibodies

&lt;400&gt; 73

agattggatg cagcatagat

20

&lt;210&gt; 74

&lt;211&gt; 457

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: DNA encoding  
the partial peptide of the heavy chain of a  
humanized anti-Fas antibody

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (21)..(455)

&lt;220&gt;

&lt;221&gt; mat peptide

&lt;222&gt; (78)..(455)

&lt;220&gt;

&lt;221&gt; sig peptide

&lt;222&gt; (21)..(77)

&lt;400&gt; 74

aagcttggct tgacctcacc atg gga tgg agc tgt atc atc ctc ttc ttg gta 53  
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val  
-15 -10

gca aca gct aca ggt gtc cac tct cag gtc caa ctg gtg cag tct ggg 101  
Ala Thr Ala Thr Gly Val His Ser Gln Val Gln Leu Val Gln Ser Gly  
-5 -1 1 5

gct gag gtc aag aag cct ggg gct tca gtg aag gtg tcc tgc aag gct 149  
Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala  
10 15 20

tct ggc tac acc ttc acc agc tac tgg atg cag tgg gta aaa cag gcc 197  
Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met Gln Trp Val Lys Gln Ala  
25 30 35 40

cct gga cag agg ctt gag tgg atg gga gag att gat cct tct gat agc 245  
Pro Gly Gln Arg Leu Glu Trp Met Gly Glu Ile Asp Pro Ser Asp Ser  
45 50 55

tat	act	aac	tac	aat	caa	aag	ttc	aag	ggc	aag	gcc	aca	ttg	act	gta	293
Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	
		60						65					70			

gac	aca	tcc	gct	agc	aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	aga	tct	341
Asp	Thr	Ser	Ala	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	
		75					80					85				

gag	gac	acg	gcg	gtc	tat	tac	tgt	gca	aga	aat	agg	gac	tat	agt	aac	389
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asn	Arg	Asp	Tyr	Ser	Asn	
	90					95					100					

aac	tgg	tac	ttc	gat	gtc	tgg	ggc	gaa	ggg	acc	ctg	gtc	acc	gtc	tcc	437
Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Glu	Gly	Thr	Leu	Val	Thr	Val	Ser	
105					110					115					120	

tca	gcc	tcc	acc	aag	ggc	cc										457
Ser	Ala	Ser	Thr	Lys	Gly											
				125												

&lt;210&gt; 75

&lt;211&gt; 145

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Designed partial  
peptide of the heavy chain of humanized anti-human  
Fas antibody

&lt;400&gt; 75

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
				-15					-10					-5		

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
	-1	1				5						10				

Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
	15					20					25					

Thr	Ser	Tyr	Trp	Met	Gln	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Arg	Leu	
	30				35					40					45	

Glu	Trp	Met	Gly	Glu	Ile	Asp	Pro	Ser	Asp	Ser	Tyr	Thr	Asn	Tyr	Asn	
			50						55						60	

Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Thr	Ser	Ala	Ser	
			65					70					75			

Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
		80					85					90				



Tyr Tyr Cys Ala Arg Asn Arg Asp Tyr Ser Asn Asn Trp Tyr Phe Asp  
           95                                  100                                  105

Val Trp Gly Glu Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
   110                                  115                                  120                                  125

Gly

<210> 76  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
           amplify a fragment of the DNA encoding variable  
           region in the heavy chain of a humanized anti-Fas  
           antibody

<400> 76  
 gggaagcttg gcttgacctc accatgggat ggagctgtat

40

<210> 77  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
           amplify a fragment of the DNA encoding variable  
           region in the heavy chain of a humanized anti-Fas  
           antibody

<400> 77  
 tgaagcccca ggcttcttga cctcagcccc agactgcacc agttggac

48

<210> 78  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to  
           amplify a fragment of the DNA encoding variable  
           region in the heavy chain of a humanized anti-Fas  
           antibody

<400> 78

tccactcaag cctctgtcca ggggcctgtt ttaccc

36

<210> 79  
 <211> 52  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of the DNA encoding variable  
 region in the heavy chain of a humanized anti-Fas  
 antibody

<400> 79  
 gtctggggct gaggtcaaga agcctggggc ttcagtgaag gtgtcctgca ag

52

<210> 80  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of the DNA encoding variable  
 region in the heavy chain of a humanized anti-Fas  
 antibody

<400> 80  
 caggccctg gacagaggct tgagtggatg ggagagatt

39

<210> 81  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of the DNA encoding variable  
 region in the heavy chain of a humanized anti-Fas  
 antibody

<400> 81  
 tcagatctca ggctgctgag ctccatgtag gctgtgctag cggatgtgtc

50

<210> 82  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of the DNA encoding variable region in the heavy chain of a humanized anti-Fas antibody

<400> 82

tggagctcag cagcctgaga tctgaggaca cggcgggtcta ttac

44

<210> 83

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of the DNA encoding variable region in the heavy chain of a humanized anti-Fas antibody

<400> 83

gatgggccct tgggtggaggc tgaggagacg gtgaccaggg tcccttcgcc ccagt

55

<210> 84

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of the DNA encoding the constant region of human immunoglobulin G1 heavy chain

<400> 84

gggaagcttc cgcggtcaca tggcaccacc tctcttgca

39

<210> 85

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of the DNA encoding the constant region of human immunoglobulin G1 heavy chain

<400> 85

gctctgcaga gagaagattg ggagttactg gaatc

35

<210> 86  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of the DNA encoding the constant region of human immunoglobulin G1 heavy chain

<400> 86  
 tctctgcaga gcccaaactct tgtgacaaaa ctcac

35

<210> 87  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of the DNA encoding the constant region of human immunoglobulin G1 heavy chain

<400> 87  
 ggggaattcg ggagcggggc ttgccggccg tcgcactca

39

<210> 88  
 <211> 2077  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed DNA encoding the heavy chain of a humanized anti-Fas antibody

<220>  
 <221> sig peptide  
 <222> (27)..(83)

<220>  
 <221> intron  
 <222> (741)..(1131)

<220>  
 <221> intron  
 <222> (1177)..(1294)

<220>  
 <221> intron

<222> (1625)..(1721)

<220>

<221> exon

<222> (27)..(740)

<220>

<221> exon

<222> (1132)..(1176)

<220>

<221> exon

<222> (1295)..(1624)

<220>

<221> exon

<222> (1722)..(2042)

<220>

<221> mat peptide

<222> (84)..(740)

<220>

<221> mat peptide

<222> (1132)..(1176)

<220>

<221> mat peptide

<222> (1295)..(1624)

<220>

<221> mat peptide

<222> (1722)..(2042)

<220>

<221> CDS

<222> (27)..(740)

<220>

<221> CDS

<222> (1132)..(1176)

<220>

<221> CDS

<222> (1295)..(1624)

<220>

<221> CDS

<222> (1722)..(2042)

<400> 88

gggcgaaagc ttggcttgac ctcacc atg gga tgg agc tgt atc atc ctc ttc 53  
Met Gly Trp Ser Cys Ile Ile Leu Phe

-15

ttg	gta	gca	aca	gct	aca	ggg	gtc	cac	tct	cag	gtc	caa	ctg	gtg	cag	101
Leu	Val	Ala	Thr	Ala	Thr	Gly	Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	
-10					-5				-1	1				5		
tct	ggg	gct	gag	gtc	aag	aag	cct	ggg	gct	tca	gtg	aag	gtg	tcc	tgc	149
Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	
			10					15					20			
aag	gct	tct	ggc	tac	acc	ttc	acc	agc	tac	tgg	atg	cag	tgg	gta	aaa	197
Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Trp	Met	Gln	Trp	Val	Lys	
		25					30					35				
cag	gcc	cct	gga	cag	agg	ctt	gag	tgg	atg	gga	gag	att	gat	cct	tct	245
Gln	Ala	Pro	Gly	Gln	Arg	Leu	Glu	Trp	Met	Gly	Glu	Ile	Asp	Pro	Ser	
	40					45					50					
gat	agc	tat	act	aac	tac	aat	caa	aag	ttc	aag	ggc	aag	gcc	aca	ttg	293
Asp	Ser	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	
55					60					65					70	
act	gta	gac	aca	tcc	gct	agc	aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	341
Thr	Val	Asp	Thr	Ser	Ala	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	
				75					80					85		
aga	tct	gag	gac	acg	gcg	gtc	tat	tac	tgt	gca	aga	aat	agg	gac	tat	389
Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asn	Arg	Asp	Tyr	
			90					95					100			
agt	aac	aac	tgg	tac	ttc	gat	gtc	tgg	ggc	gaa	ggg	acc	ctg	gtc	acc	437
Ser	Asn	Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Glu	Gly	Thr	Leu	Val	Thr	
		105					110					115				
gtc	tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	485
Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	
	120					125					130					
tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	533
Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	
135					140					145					150	
aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	581
Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	
				155					160					165		
ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	629
Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	
			170					175					180			
ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	677
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	
		185					190					195				
acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	725

Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
200 205 210

gtg gac aag aga gtt ggtgagaggg cagcacaggg agggaggggtg tctgctggaa 780  
Val Asp Lys Arg Val  
215

gccaggctca gcgctcctgc ctggacgcat cccggctatg cagtcccagt ccagggcagc 840  
aaggcaggcc ccgtctgcct cttcaccgag aggcctctgc ccgccccact catgctcagg 900  
gagaggggtct tctggctttt tccccaggct ctgggcaggc acaggctagg tgcccctaac 960  
ccaggccctg cacacaaagg ggcagggtgct gggctcagac ctgccaagag ccatatccgg 1020  
gaggaccctg cccctgacct aagcccaccc caaaggccaa actctccact ccctcagctc 1080  
ggacaccttc tctcctccca gattccagta actcccaatc ttctctctgc a gag ccc 1137  
Glu Pro  
220

aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca ggtaagccag 1186  
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
225 230

cccaggcctc gccctccagc tcaaggcggg acagggtgcc tagagtagcc tgcattccagg 1246  
gacaggcccc agccgggtgc tgacacgtcc acctccatct cttcctca gca cct gaa 1303  
Ala Pro Glu  
235

ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac 1351  
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
240 245 250

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac 1399  
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
255 260 265

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc 1447  
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
270 275 280 285

gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac 1495  
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  
290 295 300

agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg 1543  
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca 1591  
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
320 325 330

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtgggggtgcg 1644  
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
 335 340

agggccacat ggacagaggc cggctcggcc caccctctgc cctgagagtg accgctgtac 1704

caacctctgt ccctaca ggg cag ccc cga gaa cca cag gtg tac acc ctg 1754  
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
 345 350 355

ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc 1802  
 Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys  
 360 365 370

ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc 1850  
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
 375 380 385

aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac 1898  
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
 390 395 400

tcc gac ggc tcc ttc ttc ctc tat agc aag ctc acc gtg gac aag agc 1946  
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
 405 410 415

agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct 1994  
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
 420 425 430 435

ctg cac aac cac tac acg cag aag agc ctc tcc ctg tcc ccg ggt aaa 2042  
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 440 445 450

tgagtgcgac ggccggcaag ccccgctccc gaatt 2077

<210> 89

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed heavy  
 chain of humanized anti-Fas antibody

<400> 89

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 -15 -10 -5

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
 -1 1 5 10



Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
	15					20					25				
Thr	Ser	Tyr	Trp	Met	Gln	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Arg	Leu
30					35					40					45
Glu	Trp	Met	Gly	Glu	Ile	Asp	Pro	Ser	Asp	Ser	Tyr	Thr	Asn	Tyr	Asn
				50					55					60	
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Thr	Ser	Ala	Ser
			65					70					75		
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
		80					85					90			
Tyr	Tyr	Cys	Ala	Arg	Asn	Arg	Asp	Tyr	Ser	Asn	Asn	Trp	Tyr	Phe	Asp
	95					100					105				
Val	Trp	Gly	Glu	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys
110					115					120					125
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly
				130					135					140	
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro
			145					150					155		
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr
		160					165					170			
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val
	175					180					185				
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn
190					195					200					205
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro
				210					215					220	
Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu
			225					230					235		
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp
		240					245					250			
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
	255					260					265				
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly
270					275					280					285
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn
				290					295					300	

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
                   305                                  310                                  315  
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
                   320                                  325                                  330  
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
                   335                                  340                                  345  
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
                   350                                  355                                  360                                  365  
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
                                   370                                  375                                  380  
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
                                   385                                  390                                  395  
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
                   400                                  405                                  410  
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
                   415                                  420                                  425  
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
                   430                                  435                                  440                                  445  
 Ser Leu Ser Pro Gly Lys  
                                   450

<210> 90  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Sequencing  
           primer for a DNA encoding the heavy chain of a  
           humanized anti-Fas antibody

<400> 90  
 acagccggga aggtgtgcac

20

<210> 91  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Sequencing  
           primer for a DNA encoding the heavy chain of a  
           humanized anti-Fas antibody

<400> 91  
agacaccctc cctccctgtg

20

<210> 92  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequencing  
primer for a DNA encoding the heavy chain of a  
humanized anti-Fas antibody

<400> 92  
gtgcagggcc tgggttaggg

20

<210> 93  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequencing  
primer for a DNA encoding the heavy chain of a  
humanized anti-Fas antibody

<400> 93  
gcacggtggg catgtgtgag

20

<210> 94  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequencing  
primer for a DNA encoding the heavy chain of a  
humanized anti-Fas antibody

<400> 94  
gttttggggg gaagaggaag

20

<210> 95  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequencing  
primer for a DNA encoding the heavy chain of a

## humanized anti-Fas antibody

&lt;400&gt; 95

ccagtcctgg tgcaggacgg

20

&lt;210&gt; 96

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Sequencing primer for a DNA encoding the heavy chain of a humanized anti-Fas antibody

&lt;400&gt; 96

cctgtgggttc tcggggctgc

20

&lt;210&gt; 97

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Sequencing primer for a DNA encoding the heavy chain of a humanized anti-Fas antibody

&lt;400&gt; 97

cgtggtccttg tagttgttct

20

&lt;210&gt; 98

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Sequencing primer for a DNA encoding the heavy chain of a humanized anti-Fas antibody

&lt;400&gt; 98

cttcctcttc ccccaaaac

20

&lt;210&gt; 99

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Sequencing primer for a DNA encoding the heavy chain of a humanized anti-Fas antibody

<400> 99  
ccgtcctgca ccaggactgg

20

<210> 100  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequencing primer for a DNA encoding the heavy chain of a humanized anti-Fas antibody

<400> 100  
gcagccccga gaaccacagg

20

<210> 101  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequencing primer for a DNA encoding the heavy chain of a humanized anti-Fas antibody

<400> 101  
agaacaacta caagaccagc

20

<210> 102  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Sequencing primer for a DNA encoding the heavy chain of a humanized anti-Fas antibody

<400> 102  
gcctgacatc tgaggactc

19

<210> 103  
<211> 19  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Sequencing  
primer for a DNA encoding the heavy chain of a  
humanized anti-Fas antibody

&lt;400&gt; 103

gagtcctcag atgtcaggc

19

&lt;210&gt; 104

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Sequencing  
primer for a DNA encoding the heavy chain of a  
humanized anti-Fas antibody

&lt;400&gt; 104

gagcagtact cgttgctgcc gcgcgcgcca ccag

34

&lt;210&gt; 105

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Sequencing  
primer for a DNA encoding the heavy chain of a  
humanized anti-Fas antibody

&lt;400&gt; 105

ggatatggctg attaatgatc aatg

24

&lt;210&gt; 106

&lt;211&gt; 768

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Designed DNA  
encoding the light chain of a humanized anti-Fas  
antibody

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (40)..(753)

&lt;220&gt;

&lt;221&gt; mat peptide

&lt;222&gt; (100)..(753)

&lt;220&gt;

&lt;221&gt; sig peptide

&lt;222&gt; (40)..(99)

&lt;400&gt; 106

cccaagctta	agaagcatcc	tctcatctag	ttctcagag	atg	gag	aca	gac	aca		54						
				Met	Glu	Thr	Asp	Thr								
				-20												
atc	ctg	cta	tgg	gtg	ctg	ctg	ctc	tgg	gtt	cca	ggc	tcc	act	ggg	gag	102
Ile	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro	Gly	Ser	Thr	Gly	Glu	
-15					-10					-5				-1	1	
att	gtg	ctc	acc	caa	tct	cca	ggg	act	ttg	tct	ctg	tct	cca	ggg	gag	150
Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	Leu	Ser	Pro	Gly	Glu	
			5					10					15			
agg	gcc	acc	ctc	tcc	tgc	aag	gcc	agc	caa	agt	gtt	gat	tat	gat	ggg	198
Arg	Ala	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp	Gly	
		20					25					30				
gat	agt	tat	atg	aac	tgg	tac	caa	cag	aaa	cca	gga	cag	gca	ccc	aga	246
Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	
	35					40					45					
ctc	ctc	atc	tat	gct	gca	tcc	aac	ctc	gaa	tct	ggg	atc	cca	gac	agg	294
Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Asp	Arg	
50					55					60					65	
ttt	agt	ggc	agt	ggg	tct	ggg	aca	gac	ttc	acc	ctc	acc	atc	tct	cgt	342
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Arg	
				70					75					80		
ctg	gag	ccg	gag	gat	ttt	gca	gtc	tat	tac	tgt	cag	caa	agt	aac	gag	390
Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn	Glu	
			85					90					95			
gat	cct	cgg	acg	ttc	ggg	caa	ggc	acc	aag	ctg	gaa	atc	aaa	cgg	act	438
Asp	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	
		100					105					110				
gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	cag	ttg	486
Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	
	115					120					125					
aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aac	aac	ttc	tat	ccc	534
Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	
130					135				140						145	
aga	gag	gcc	aaa	gta	cag	tgg	aaa	gtg	gat	aac	gcc	ctc	caa	tcg	ggg	582
Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	
				150					155					160		
aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	agc	aag	gac	agc	acc	tac	630

Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr		
			165					170					175				
agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	gca	gac	tac	gag	aaa	cac	678	
Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His		
		180					185					190					
aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	ggc	ctg	agc	tcg	ccc	gtc	726	
Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val		
	195					200					205						
aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tagtaagaat	tcggg						768	
Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys									
210					215												

&lt;210&gt; 107

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: Designed light chain of humanized anti-Fas antibody

&lt;400&gt; 107

Met	Glu	Thr	Asp	Thr	Ile	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro		
-20					-15					-10					-5		
Gly	Ser	Thr	Gly	Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser		
			-1	1				5					10				
Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gln	Ser		
		15					20					25					
Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro		
	30					35					40						
Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser		
45					50				55						60		
Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr		
				65					70					75			
Leu	Thr	Ile	Ser	Arg	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Val	Tyr	Tyr	Cys		
			80					85					90				
Gln	Gln	Ser	Asn	Glu	Asp	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu		
		95					100					105					
Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro		
	110					115						120					



Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
 125 130 135 140  
 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
 145 150 155  
 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
 160 165 170  
 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala  
 175 180 185  
 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
 190 195 200  
 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
 205 210 215 6 7 8

<210> 108  
 <211> 768  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (40)..(753)

<220>  
 <221> mat peptide  
 <222> (100)..(753)

<220>  
 <221> sig peptide  
 <222> (40)..(99)

<220>  
 <223> Description of Artificial Sequence: Designed DNA  
 encoding the light chain of a humanized anti-Fas  
 antibody

<400> 108  
 cccaagctta agaagcatcc tctcatctag ttctcagag atg gag aca gac aca 54  
 Met Glu Thr Asp Thr  
 -20  
 atc ctg cta tgg gtg ctg ctg ctc tgg gtt cca ggc tcc act ggt gag 102  
 Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser Thr Gly Glu  
 -15 -10 -5 -1 1  
 att gtg ctc acc caa tct cca ggt act ttg tct ctg tct cca ggg gag 150  
 Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly Glu  
 5 10 15

agg	gcc	acc	ctc	tcc	tgc	aag	gcc	agc	caa	agt	gtt	gat	tat	gat	ggt	198
Arg	Ala	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gln	Ser	Val	Asp	Tyr	Asp	Gly	
		20					25					30				
gat	agt	tat	atg	aac	tgg	tac	caa	cag	aaa	cca	gga	cag	gca	ccc	aga	246
Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Arg	
	35					40					45					
ctc	ctc	atc	tat	gct	gca	tcc	aat	ctc	gaa	tct	ggg	atc	cca	gac	agg	294
Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Asp	Arg	
	50				55					60					65	
ttt	agt	ggc	agt	ggg	tct	ggg	aca	gac	ttc	acc	ctc	acc	atc	cat	cct	342
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	His	Pro	
				70					75					80		
gtg	gag	gag	gag	gat	gct	gca	acc	tat	tac	tgt	cag	caa	agt	aat	gag	390
Val	Glu	Glu	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn	Glu	
			85					90					95			
gat	cct	cgg	acg	ttc	ggt	caa	ggc	acc	aag	ctg	gaa	atc	aaa	cgg	act	438
Asp	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Arg	Thr	
		100					105					110				
gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	cag	ttg	486
Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	
	115					120					125					
aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	ttc	tat	ccc	534
Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	
	130				135				140						145	
aga	gag	gcc	aaa	gta	cag	tgg	aaa	gtg	gat	aac	gcc	ctc	caa	tcg	ggt	582
Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	
				150					155					160		
aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	agc	aag	gac	agc	acc	tac	630
Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	
			165					170					175			
agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	gca	gac	tac	gag	aaa	cac	678
Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	
		180					185					190				
aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	ggc	ctg	agc	tcg	ccc	gtc	726
Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	
	195					200					205					
aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tagtaagaat	tcggg						768
Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys								
	210				215											

&lt;210&gt; 109

<211> 238  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed light chain of humanized anti-Fas antibody

<400> 109

Met	Glu	Thr	Asp	Thr	Ile	Leu	Leu	Trp	Val	Leu	Leu	Leu	Trp	Val	Pro	-20	-15	-10	-5
Gly	Ser	Thr	Gly	Glu	Ile	Val	Leu	Thr	Gln	Ser	Pro	Gly	Thr	Leu	Ser	-1	1	5	10
Leu	Ser	Pro	Gly	Glu	Arg	Ala	Thr	Leu	Ser	Cys	Lys	Ala	Ser	Gln	Ser	15	20	25	
Val	Asp	Tyr	Asp	Gly	Asp	Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	30	35	40	
Gly	Gln	Ala	Pro	Arg	Leu	Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	45	50	55	60
Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	65	70	75	
Leu	Thr	Ile	His	Pro	Val	Glu	Glu	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	80	85	90	
Gln	Gln	Ser	Asn	Glu	Asp	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	95	100	105	
Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	110	115	120	
Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	125	130	135	140
Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	145	150	155	
Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	160	165	170	
Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	175	180	185	
Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	190	195	200	
Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys			205	210	215	

<210> 110  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of a DNA encoding the light chain of a humanized anti-Fas antibody

<400> 110  
 ggtgagattg tgctcaccca atctccagg

29

<210> 111  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of a DNA encoding the light chain of a humanized anti-Fas antibody

<400> 111  
 cctggagatt gggtgagcac aatctcacc

29

<210> 112  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of a DNA encoding the light chain of a humanized anti-Fas antibody

<400> 112  
 ccattctctcg tctggagccg gaggattttg c

31

<210> 113  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of a DNA encoding the light chain of a humanized anti-Fas antibody

<400> 113  
 gcaaaatcct ccggtccag acgagagatg g

31

<210> 114  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of a DNA encoding the light  
 chain of a humanized anti-Fas antibody

<400> 114  
 caaggcacca agctggaaat caaacggact g

31

<210> 115  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of a DNA encoding the light  
 chain of a humanized anti-Fas antibody

<400> 115  
 cagtccgttt gatttccagc ttggtgcctt g

31

<210> 116  
 <211> 2071  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Designed DNA  
 encoding the heavy chain of a humanized anti-Fas  
 antibody

<220>  
 <221> sig peptide  
 <222> (21)..(77)

<220>  
 <221> intron  
 <222> (735)..(1125)

<220>  
 <221> intron  
 <222> (1171)..(1288)

<220>  
 <221> intron  
 <222> (1619)..(1715)



Ala	Thr	Ala	Thr	Gly	Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly		
			-5				-1	1				5					
gct	gag	gtc	aag	aag	cct	ggg	gct	tca	gtg	aag	gtg	tcc	tgc	aag	gct	149	
Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala		
10						15					20						
tct	ggc	tac	acc	ttc	acc	agc	tac	tgg	atg	cag	tgg	gta	aaa	cag	gcc	197	
Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Trp	Met	Gln	Trp	Val	Lys	Gln	Ala		
25					30					35					40		
cct	gga	cag	ggc	ctt	gag	tgg	atg	gga	gag	att	gat	cct	tct	gat	agc	245	
Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Glu	Ile	Asp	Pro	Ser	Asp	Ser		
				45					50					55			
tat	act	aac	tac	aat	caa	aag	ttc	aag	ggc	aag	gcc	aca	ttg	act	gta	293	
Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val		
			60					65					70				
gac	aca	tcc	act	agc	aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	aga	tct	341	
Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser		
		75					80					85					
gag	gac	acg	gcg	gtc	tat	tac	tgt	gca	aga	aat	agg	gac	tat	agt	aac	389	
Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asn	Arg	Asp	Tyr	Ser	Asn		
	90					95					100						
aac	tgg	tac	ttc	gat	gtc	tgg	ggc	gaa	ggg	acc	ctg	gtc	acc	gtc	tcc	437	
Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Glu	Gly	Thr	Leu	Val	Thr	Val	Ser		
105					110					115					120		
tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	tcc	485	
Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser		
				125					130					135			
aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	gac	533	
Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp		
			140					145					150				
tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	acc	581	
Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr		
		155					160					165					
agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	tac	629	
Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr		
	170					175					180						
tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	cag	677	
Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln		
185					190				195						200		
acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	gac	725	
Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp		
				205					210					215			

aag aga gtt ggtgagaggg cagcacaggg agggaggggtg tctgctggaa  
Lys Arg Val

774

gccagggtca gcgctcctgc ctggacgcat cccggctatg cagtcccagt ccagggcagc 834

aaggcaggcc ccgtctgcct cttcaccgag aggcctctgc ccgccccact catgctcagg 894

gagaggggtct tctggctttt tccccaggct ctgggcaggc acaggctagg tgcccctaac 954

ccaggccctg cacacaaagg ggcagggtgt gggctcagac ctgccaagag ccatatccgg 1014

gaggaccctg cccctgacct aagcccaccc caaaggccaa actctccact ccctcagctc 1074

ggacaccttc tctctccca gattccagta actcccaatc ttctctctgc a gag ccc 1131  
Glu Pro  
220

aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca ggtaagccag 1180  
Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
225 230

cccaggcctc gccctccagc tcaaggcggg acagggtgcc tagagtagcc tgcattccagg 1240

gacaggcccc agccgggtgc tgacacgtcc acctccatct cttcctca gca cct gaa 1297  
Ala Pro Glu  
235

ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac 1345  
Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
240 245 250

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac 1393  
Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
255 260 265

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc 1441  
Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
270 275 280 285

gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac 1489  
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  
290 295 300

agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg 1537  
Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca 1585  
Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
320 325 330

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtgggggtgcg 1638  
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
335 340



agggccacat ggacagagggc cggctcggcc caccctctgc cctgagagtg accgctgtac 1698  
 caacctctgt ccctaca ggg cag ccc cga gaa cca cag gtg tac acc ctg 1748  
                   Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
                   345                  350                  355  
 ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc 1796  
 Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys  
                   360                  365                  370  
 ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc 1844  
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
                   375                  380                  385  
 aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac 1892  
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
                   390                  395                  400  
 tcc gac ggc tcc ttc ttc ctc tat agc aag ctc acc gtg gac aag agc 1940  
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
                   405                  410                  415  
 agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct 1988  
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
                   420                  425                  430                  435  
 ctg cac aac cac tac acg cag aag agc ctc tcc ctg tcc ccg ggt aaa 2036  
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
                   440                  445                  450  
 tgagtgcgac ggccggcaag ccccgctccc gaatt 2071

<210> 117  
 <211> 470  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Designed heavy  
           chain of humanized anti-Fas antibody

<400> 117  
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
                   -15                  -10                  -5  
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
                   -1   1                  5                  10  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
           15                  20                  25

Thr Ser Tyr Trp Met Gln Trp Val Lys Gln Ala Pro Gly Gln Gly Leu  
 30 35 40 45  
 Glu Trp Met Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn  
 50 55 60  
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Ser  
 65 70 75  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
 80 85 90  
 Tyr Tyr Cys Ala Arg Asn Arg Asp Tyr Ser Asn Asn Trp Tyr Phe Asp  
 95 100 105  
 Val Trp Gly Glu Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
 110 115 120 125  
 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
 130 135 140  
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 145 150 155  
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 160 165 170  
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
 175 180 185  
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
 190 195 200 205  
 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro  
 210 215 220  
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
 225 230 235  
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 240 245 250  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 255 260 265  
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 270 275 280 285  
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  
 290 295 300  
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 305 310 315

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
           320                          325                          330  
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
           335                          340                          345  
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
   350                          355                          360                          365  
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
                           370                          375                          380  
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
                           385                          390                          395  
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
           400                          405                          410  
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
           415                          420                          425  
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
   430                          435                          440                          445  
 Ser Leu Ser Pro Gly Lys  
                           450

<210> 118  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of a DNA encoding the heavy  
 chain of a humanized anti-Fas antibody

<400> 118  
 caggcccctg gacagggcct tgagtggatg

30

<210> 119  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of a DNA encoding the heavy  
 chain of a humanized anti-Fas antibody

<400> 119  
 catccactca aggcctgtc caggggcctg

30

<210> 120  
 <211> 39  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of a DNA encoding the heavy  
 chain of a humanized anti-Fas antibody

<400> 120  
 gctgagctcc atgtaggctg tgctagtgga tgtgtctac

39

<210> 121  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a DNA fragment including SR alpha promoter

<400> 121  
 tgcacgcgtg gctgtggaat gtgtgtcagt tag

33

<210> 122  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a DNA fragment including SR alpha promoter

<400> 122  
 tccgaagctt ttagagcaga agtaacactt c

31

<210> 123  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a DNA fragment including SR alpha promoter

<400> 123  
 aaagcggccg ctgctagctt ggctgtggaa tgtgtg

36

<210> 124  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to  
 amplify a DNA encoding the kappa light chain of  
 human immunoglobulin

<400> 124  
 aagcttatgg acatgagggt ccccgctctg ctcc

34

<210> 125  
 <211> 729  
 <212> DNA  
 <213> Homo sapiens

<400> 125  
 aagcttatgg acatgagggt ccccgctctg ctccctggggc tccctgctact ctggctccga 60  
 ggtgccagat gtgacatcca gatgaccag tctccatcct cccctgtctgc atctgtagga 120  
 gacagagtca ccatcacttg cgggcaagt cagagcatta gcagctatct aaattgggtat 180  
 cagcagaaac cagggaaagc ccctaagctc ctgatctatg ctgcatccag ttgcaaagt 240  
 ggggtcccat caagggttcag tggcagtga tctgggacag atttcaactct caccatcagc 300  
 agtctgcaac ctgaagattt tgcaacttac tactgtcaac agagttacag taccctcga 360  
 acgttcggcc aagggaacaa ggtggaaatc aaacgaactg tggctgcacc atctgtcttc 420  
 atcttcccgc catctgatga gcagttgaaa tctggaactg cctctgttgt gtgcctgctg 480  
 aataacttct atcccagaga ggccaaagta cagtggaagg tggataacgc cctccaatcg 540  
 ggtaactccc aggagagtgt tacagagcag gacagcaagg acagcaccta cagcctcagc 600  
 agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 660  
 acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgttagtaa 720  
 gaattcggg

729

<210> 126  
 <211> 767  
 <212> DNA  
 <213> Artificial Sequence

<400> 126																	56
ccaagcttaa gaagcatcct ctcatctagt tctcagag atg gag aca gac aca atc																	
Met Glu Thr Asp Thr Ile																	
-20 -15																	
ctg cta tgg gtg ctg ctg ctc tgg gtt cca ggc tcc act ggt gac att																	104
Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser Thr Gly Asp Ile																	
-10 -5 -1 1																	
gtg ctc acc caa tct cca tcc tcc ctg tct gca tct gta gga gac aga																	152
Val Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg																	
5 10 15																	
gtc acc atc act tgc aag gcc agc caa agt gtt gat tat gat ggt gat																	200
Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp																	
20 25 30																	
agt tat atg aac tgg tac caa cag aaa cca gga aag gca ccc aag ctc																	248
Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu																	
35 40 45 50																	
ctc atc tat gct gca tcc aat ttg gaa agt ggg gtc cca tca agg ttc																	296
Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Val Pro Ser Arg Phe																	
55 60 65																	
agt gga agt gga tct ggg aca gat ttt act ctc acc atc agc agc ctg																	344
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu																	
70 75 80																	
cag cct gaa gat ttt gca acc tac tac tgt cag caa agt aac gag gat																	392
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp																	
85 90 95																	
cct cgg acg ttc ggc caa ggc acc aag gtg gaa atc aaa cgg act gtg																	440
Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val																	
100 105 110																	

gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 488  
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
 115 120 125 130

tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 536  
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
 135 140 145

gag gcc aaa gta cag tgg aaa gtg gat aac gcc ctc caa tcg ggt aac 584  
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
 150 155 160

tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 632  
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
 165 170 175

ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 680  
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
 180 185 190

gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 728  
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
 195 200 205 210

aag agc ttc aac agg gga gag tgt tagtaagaat tcggg 767  
 Lys Ser Phe Asn Arg Gly Glu Cys  
 215

<210> 127

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed light  
 chain of humanized anti-Fas antibody

<400> 127

Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 -20 -15 -10 -5

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser  
 -1 1 5 10

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser  
 15 20 25

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro  
 30 35 40

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser  
 45 50 55 60

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
                                 65                                70                                75  
 Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys  
                                 80                                85                                90  
 Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val  
                                 95                                100                                105  
 Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
                 110                                115                                120  
 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
                 125                                130                                135                                140  
 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
                                 145                                150                                155  
 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
                                 160                                165                                170  
 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala  
                 175                                180                                185  
 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
                 190                                195                                200  
 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
                 205                                210                                215

<210> 128  
 <211> 767  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Designed DNA  
 encoding the light chain of a humanized anti-Fas  
 antibody

<220>  
 <221> CDS  
 <222> (39)..(752)

<220>  
 <221> mat peptide  
 <222> (99)..(752)

<220>  
 <221> sig peptide  
 <222> (39)..(98)

<400> 128



ccaagcttaa gaagcatcct ctcacttagt tctcagag atg gag aca gac aca atc 56  
Met Glu Thr Asp Thr Ile  
-20 -15

ctg cta tgg gtg ctg ctg ctc tgg gtt cca ggc tcc act ggt gac att 104  
Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser Thr Gly Asp Ile  
-10 -5 -1 1

gtg ctc acc caa tct cca tcc tcc ctg tct gca tct gta gga gac aga 152  
Val Leu Thr 5 Gln Ser Pro Ser Ser 10 Leu Ser Ala Ser Val Gly Asp Arg 15

gtc acc atc act tgc aag gcc agc caa agt gtt gat tat gat ggt gat 200  
Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp  
20 25 30

agt tat atg aac tgg tac caa cag aaa cca gga cag gca ccc aag ctc 248  
Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Lys Leu  
35 40 45 50

ctc atc tat gct gca tcc aat ttg gaa agt ggg gtc cca tca agg ttc 296  
Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser Gly Val Pro Ser Arg Phe  
55 60 65

agt gga agt gga tct ggg aca gat ttt act ctc acc atc agc agc ctg 344  
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu  
70 75 80

cag cct gaa gat ttt gca acc tac tac tgt caa cag agt aac gag gat 392  
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp  
85 90 95

cct cga acg ttc ggc caa ggc acc aag gtg gaa atc aaa cgg act gtg 440  
Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val  
100 105 110

gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 488  
Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
115 120 125 130

tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 536  
Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
135 140 145

gag gcc aaa gta cag tgg aaa gtg gat aac gcc ctc caa tcg ggt aac 584  
Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
150 155 160

tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 632  
Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
165 170 175

ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 680

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
 180 185 190

gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca  
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
 195 200 205 210

728

aag agc ttc aac agg gga gag tgt tagtaagaat tcggg  
 Lys Ser Phe Asn Arg Gly Glu Cys  
 215

767

<210> 129  
 <211> 238  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Designed light  
 chain of humanized anti-Fas antibody

<400> 129  
 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro  
 -20 -15 -10 -5

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser  
 -1 1 5 10

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser  
 15 20 25

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro  
 30 35 40

Gly Gln Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser  
 45 50 55 60

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
 65 70 75

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys  
 -80 85 90

Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val  
 95 100 105

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro  
 110 115 120

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu  
 125 130 135 140

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn  
 145 150 155

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser  
                   160                  165                  170

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala  
           175                  180                  185

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly  
       190                  195                  200

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
   205                  210                  215

<210> 130  
 <211> 778  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Designed DNA  
       encoding the light chain of a humanized anti-Fas  
       antibody

<220>  
 <221> CDS  
 <222> (39)..(752)

<220>  
 <221> mat peptide  
 <222> (99)..(752)

<220>  
 <221> sig peptide  
 <222> (39)..(98)

<400> 130  
 ccaagcttaa gaagcatcct ctcacttagt tctcagag atg gag aca gac aca atc 56  
   Met Glu Thr Asp Thr Ile  
   -20                  -15

ctg cta tgg gtg ctg ctg ctc tgg gtt cca ggc tcc act ggt gac att 104  
 Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser Thr Gly Asp Ile  
                   -10                  -5                  -1      1

gtg ctc acc caa tct cca tcc tcc ctg tct gca tct gta gga gac aga 152  
 Val Leu Thr          Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg  
                   5                          10                  15

gtc acc atc act tgc aag gcc agc caa agt gtt gat tat gat ggt gat 200  
 Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Asp Tyr Asp Gly Asp  
       20                  25                  30

agt tat atg aac tgg tac caa cag aaa cca gga aag gca ccc aaa ctc 248

Ser	Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu		
35					40					45					50		
ctc	atc	tac	gct	gca	tcc	aat	ttg	gaa	tca	ggg	atc	cca	tca	agg	ttc	296	
Leu	Ile	Tyr	Ala	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Ser	Arg	Phe		
				55				60						65			
agt	gga	agt	gga	tct	ggg	aca	gat	ttt	act	ctc	acc	atc	agc	agc	ctg	344	
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu		
			70					75					80				
cag	cct	gag	gat	ttt	gca	acc	tat	tac	tgt	cag	caa	agt	aat	gag	gat	392	
Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn	Glu	Asp		
		85					90					95					
cct	cgg	acg	ttc	ggg	caa	ggc	acc	aag	gtg	gaa	atc	aaa	cgg	act	gtg	440	
Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val		
	100					105					110						
gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	cca	tct	gat	gag	cag	ttg	aaa	488	
Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys		
115				120						125				130			
tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	ctg	aat	aac	ttc	tat	ccc	aga	536	
Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg		
				135				140						145			
gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	aac	gcc	ctc	caa	tcg	ggg	aac	584	
Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn		
			150					155					160				
tcc	cag	gag	agt	gtc	aca	gag	cag	gac	agc	aag	gac	agc	acc	tac	agc	632	
Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser		
		165				170						175					
ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	gca	gac	tac	gag	aaa	cac	aaa	680	
Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys		
	180					185					190						
gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	ggc	ctg	agc	tcg	ccc	gtc	aca	728	
Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr		
195				200					205					210			
aag	agc	ttc	aac	agg	gga	gag	tgt	tagtaagaat	tcgggaagcc	gaattc						778	
Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys										
				215													

&lt;210&gt; 131

&lt;211&gt; 238

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Designed light chain of humanized anti-Fas antibody

<400> 131

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Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
-20                               -15                -10                -5

Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ser Ser Leu Ser
          -1    1                      5                      10

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser
          15                20                25

Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
          30                35                40

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
          45                50                55                60

Gly Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
          65                70                75

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
          80                85                90

Gln Gln Ser Asn Glu Asp Pro Arg Thr Phe Gly Gln Gly Thr Lys Val
          95                100               105

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
          110               115                120

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
          125                130                135                140

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
          145                150                155

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
          160                165                170

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
          175                180                185

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
          190                195                200

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
          205                210                215

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<210> 132

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody

<400> 132

agggaggatg gagattgggt gagcacaatg tcaccagtgg a

41

<210> 133

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody

<400> 133

attgtgctca cccaatctcc atcctccctg tctgcatct

39

<210> 134

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody

<400> 134

atcaacactt tggctggcct tgcaagtgat ggtgactctg tc

42

<210> 135

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to amplify a fragment of DNA encoding the light chain of a humanized anti-Fas antibody

<400> 135

ccatcacttg caaggccagc caaagtgttg attatgatgg

40

<210> 136  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of DNA encoding the light chain  
 of a humanized anti-Fas antibody

<400> 136  
 agtttcgaga ttggatgcag catagatgag gagtttgggt gcctttcc

48

<210> 137  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of DNA encoding the light chain  
 of a humanized anti-Fas antibody

<400> 137  
 cccaagctcc tcattctatgc tgcattccaat ttggaaagtg gggtc

45

<210> 138  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of DNA encoding the light chain  
 of a humanized anti-Fas antibody

<400> 138  
 ttggccgaac gttcgaggat cctcgttact ctgttgacag tagt

44

<210> 139  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of DNA encoding the light chain  
 of a humanized anti-Fas antibody

<400> 139

actactgtca acagagtaac gaggatcctc gaacgttcgg ccaa

44

<210> 140  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of DNA encoding the light chain  
 of a humanized anti-Fas antibody

<400> 140  
 ctcatctatg ctgcatccaa tttggaaagt gggatcccat caagg

45

<210> 141  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of DNA encoding the light chain  
 of a humanized anti-Fas antibody

<400> 141  
 attggatgca gcatagatga ggagcttggg tgcctgtcct ggttt

45

<210> 142  
 <211> 2073  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed DNA  
 encoding the heavy chain of a humanized anti-Fas  
 antibody

<220>  
 <221> sig peptide  
 <222> (23)..(79)

<220>  
 <221> intron  
 <222> (737)..(1127)

<220>  
 <221> intron  
 <222> (1173)..(1290)



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<220>
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<222> (1621)..(1717)

<220>
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<220>
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<222> (1128)..(1172)

<220>
<221> exon
<222> (1291)..(1620)

<220>
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<222> (1718)..(2038)

<220>
<221> mat peptide
<222> (80)..(736)

<220>
<221> mat peptide
<222> (1128)..(1172)

<220>
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<222> (1291)..(1620)

<220>
<221> mat peptide
<222> (1718)..(2038)

<220>
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<222> (23)..(736)

<220>
<221> CDS
<222> (1128)..(1172)

<220>
<221> CDS
<222> (1291)..(1620)

<220>
<221> CDS
<222> (1718)..(2038)

<400> 142

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ccaagcttgg cttgacctca cc atg gga tgg agc tgt atc atc ctc ttc ttg 52  
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu  
-15 -10

gta gca aca gct aca ggt gtc cat tct cag gtc caa ctg gtg cag tct 100  
Val Ala Thr Ala Thr Gly Val His Ser Gln Val Gln Leu Val Gln Ser  
-5 -1 1 5

ggg gct gag gtc aag aag cct ggg gct tca gtg aag gtg tcc tgc aag 148  
Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys  
10 15 20

gct tct ggc tac acc ttc acc agc tac tgg atg cag tgg gta aaa cag 196  
Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met Gln Trp Val Lys Gln  
25 30 35

gcc cct gga cag gga ctt gag tgg atg gga gag att gat cct tct gat 244  
Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Glu Ile Asp Pro Ser Asp  
40 45 50 55

agc tat act aac tac aat caa aag ttc aag ggc aag gcc aca ttg act 292  
Ser Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr  
60 65 70

gta gac aca tcc act agc aca gcc tac atg gag ctc agc agc ctg aga 340  
Val Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg  
75 80 85

tct gag gac acg gcg gtc tat tac tgt gca aga aat agg gac tat agt 388  
Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Arg Asp Tyr Ser  
90 95 100

aac aac tgg tac ttc gat gtc tgg ggc caa ggt aca ctg gtc acc gtc 436  
Asn Asn Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val  
105 110 115

tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc 484  
Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser  
120 125 130 135

tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag 532  
Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys  
140 145 150

gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg 580  
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu  
155 160 165

acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc 628  
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu  
170 175 180

tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc 676

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
 185 190 195  
 cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg 724  
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
 200 205 210 215  
 gac aag aga gtt ggtgagagggc cagcacaggg agggaggggtg tctgctggaa 776  
 Asp Lys Arg Val  
 gccagggtca gcgctcctgc ctggacgcat cccggctatg cagtcccagt ccagggcagc 836  
 aaggcaggcc ccgtctgcct cttcaccgag aggcctctgc ccgccccact catgctcagg 896  
 gagaggggtct tctggctttt tccccaggct ctgggcaggc acaggctagg tgcccctaac 956  
 ccaggccctg cacacaaagg ggcagggtgct gggctcagac ctgccaagag ccatatccgg 1016  
 gaggaccctg cccctgacct aagcccaccc caaaggccaa actctccact ccctcagctc 1076  
 ggacaccttc tctcctccca gattccagta actcccaatc ttctctctgc a gag ccc 1133  
 Glu Pro  
 220  
 aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca ggtaagccag 1182  
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
 225 230  
 cccaggcctc gccctccagc tcaaggcggg acagggtgcc tagagtagcc tgcattccagg 1242  
 gacaggcccc agccgggtgc tgacacgtcc acctccatct cttcctca gca cct gaa 1299  
 Ala Pro Glu  
 235  
 ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac 1347  
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 240 245 250  
 acc ctc atg atc tcc ccg acc cct gag gtc aca tgc gtg gtg gtg gac 1395  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 255 260 265  
 gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc 1443  
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 270 275 280 285  
 gtg gag gtg cat aat gcc aag aca aag ccg ccg gag gag cag tac aac 1491  
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  
 290 295 300  
 agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg 1539  
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 305 310 315

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca 1587  
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
           320                                  325                                  330

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtgggggtgcg 1640  
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
           335                                  340

agggccacat ggacagaggc cggctcggcc caccctctgc cctgagagtg accgctgtac 1700

caacctctgt ccctaca ggg cag ccc cga gaa cca cag gtg tac acc ctg 1750  
                                   Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
                                   345                                  350                                  355

ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc 1798  
 Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys  
                                   360                                  365                                  370

ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc 1846  
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
                                   375                                  380                                  385

aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac 1894  
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
                                   390                                  395                                  400

tcc gac ggc tcc ttc ttc ctc tat agc aag ctc acc gtg gac aag agc 1942  
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
           405                                  410                                  415

agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct 1990  
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
           420                                  425                                  430                                  435

ctg cac aac cac tac acg cag aag agc ctc tcc ctg tcc ccg ggt aaa 2038  
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
                                   440                                  445                                  450

tgagtgcgac ggccggcaag ccccgctccc gaatt 2073

<210> 143  
 <211> 470  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Designed heavy  
           chain of humanized anti-Fas antibody

<400> 143  
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
                                   -15                                  -10                                  -5

Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
                   -1     1                         5                         10  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
           15                         20                         25  
 Thr Ser Tyr Trp Met Gln Trp Val Lys Gln Ala Pro Gly Gln Gly Leu  
   30                         35                         40                         45  
 Glu Trp Met Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn  
                   50                         55                         60  
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Ser  
                   65                         70                         75  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
                   80                         85                         90  
 Tyr Tyr Cys Ala Arg Asn Arg Asp Tyr Ser Asn Asn Trp Tyr Phe Asp  
           95                         100                         105  
 Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
  110                         115                         120  
 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
                   130                         135                         140  
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
                   145                         150                         155  
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
           160                         165                         170  
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
           175                         180                         185  
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
  190                         195                         200  
 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro  
                   210                         215                         220  
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
                   225                         230                         235  
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
           240                         245                         250  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
           255                         260                         265  
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
  270                         275                         280                         285

325

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  
290 295 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
305 310 315

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
320 325 330

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
335 340 345

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
350 355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
385 390 395

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
400 405 410

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
415 420 425

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
430 435 440 445

Ser Leu Ser Pro Gly Lys  
450

<210> 144

<211> 2073

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed DNA  
encoding the heavy chain of a humanized anti-Fas  
antibody

<220>

<221> sig peptide

<222> (23)..(79)

<220>

<221> intron

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<222> (1291)..(1620)

<220>

<221> CDS

<222> (1718)..(2038)

&lt;400&gt; 144

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			Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu				
							-15					-10				
gta	gca	aca	gct	aca	ggg	gtc	cat	tct	cag	gtc	caa	ctg	gtg	cag	tct	100
Val	Ala	Thr	Ala	Thr	Gly	Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	
				-5				-1	1				5			
ggg	gct	gag	gtc	aag	aag	cct	ggg	gct	tca	gtg	aag	gtg	tcc	tgc	aag	148
Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	
		10					15					20				
gct	tct	ggc	tac	acc	ttc	acc	agc	tac	tgg	atg	cag	tgg	gta	aaa	cag	196
Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Trp	Met	Gln	Trp	Val	Lys	Gln	
	25					30					35					
gcc	cct	gga	cag	gga	ctt	gag	tgg	atg	gga	gag	att	gat	cct	tct	gat	244
Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Glu	Ile	Asp	Pro	Ser	Asp	
40					45					50					55	
agc	tat	act	aac	tac	aat	caa	aag	ttc	aag	ggc	aag	gcc	aca	ata	act	292
Ser	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Ile	Thr	
				60					65					70		
gta	gac	aca	tcc	act	agc	aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	aga	340
Val	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	
			75					80					85			
tct	gag	gac	acg	gcg	gtc	tat	tac	tgt	gca	aga	aat	agg	gac	tat	agt	388
Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asn	Arg	Asp	Tyr	Ser	
		90					95					100				
aac	aac	tgg	tac	ttc	gat	gtc	tgg	ggc	caa	ggg	aca	ctg	gtc	acc	gtc	436
Asn	Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	
105						110					115					
tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	484
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
120					125					130					135	
tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	532
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
				140					145					150		
gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	580
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
			155					160					165			
acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	628
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
		170					175					180				
tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	676



Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
 185 190 195  
 cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg 724  
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
 200 205 210 215  
 gac aag aga gtt ggtgagagggc cagcacaggg agggaggggtg tctgctggaa 776  
 Asp Lys Arg Val  
 gccaggctca gcgctcctgc ctggacgcat cccggctatg cagtcccagt ccagggcagc 836  
 aaggcaggcc ccgtctgcct cttcaccceg aggcctctgc ccgccccact catgctcagg 896  
 gagaggggtct tctggctttt tccccagggt ctgggcaggc acaggctagg tgcccctaac 956  
 ccaggccctg cacacaaagg ggcaggtgct gggctcagac ctgccaagag ccatatccgg 1016  
 gaggaccctg cccctgacct aagcccaccc caaaggccaa actctccact cctcagctc 1076  
 ggacaccttc tctcctccca gattccagta actcccaatc ttctctctgc a gag ccc 1133  
 Glu Pro  
 220  
 aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca ggtaagccag 1182  
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
 225 230  
 cccaggcctc gccctccagc tcaaggcggg acagggtgcc tagagtagcc tgcattccagg 1242  
 gaagggcccc agccgggtgc tgacacgtcc acctccatct cttcctca gca cct gaa 1299  
 Ala Pro Glu  
 235  
 ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac 1347  
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 240 245 250  
 acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac 1395  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 255 260 265  
 gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc 1443  
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 270 275 280 285  
 gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac 1491  
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  
 290 295 300  
 agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg 1539  
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 305 310 315

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca 1587  
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
           320                                  325                                  330

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtgggggtgcg 1640  
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
           335                                  340

agggccacat ggacagagggc cggctcggcc caccctctgc cctgagagtg accgctgtac 1700

caacctctgt ccctaca ggg cag ccc cga gaa cca cag gtg tac acc ctg 1750  
                   Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
                   345                                  350                                  355

ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc 1798  
 Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys  
                   360                                  365                                  370

ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc 1846  
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
                   375                                  380                                  385

aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac 1894  
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
                   390                                  395                                  400

tcc gac ggc tcc ttc ttc ctc tat agc aag ctc acc gtg gac aag agc 1942  
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
           405                                  410                                  415

agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct 1990  
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
           420                                  425                                  430                                  435

ctg cac aac cac tac acg cag aag agc ctc tcc ctg tcc ccg ggt aaa 2038  
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
                   440                                  445                                  450

tgagtgcgac ggccggcaag ccccgtctcc gaatt 2073

<210> 145

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Designed heavy  
 chain of humanized anti-Fas antibody

<400> 145

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
                   -15                                  -10                                  -5

Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys
		-1	1				5					10			
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
	15					20					25				
Thr	Ser	Tyr	Trp	Met	Gln	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Gly	Leu
30					35					40					45
Glu	Trp	Met	Gly	Glu	Ile	Asp	Pro	Ser	Asp	Ser	Tyr	Thr	Asn	Tyr	Asn
				50					55					60	
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Ile	Thr	Val	Asp	Thr	Ser	Thr	Ser
			65					70					75		
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val
		80					85					90			
Tyr	Tyr	Cys	Ala	Arg	Asn	Arg	Asp	Tyr	Ser	Asn	Asn	Trp	Tyr	Phe	Asp
	95					100					105				
Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys
110					115					120					125
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly
				130					135					140	
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro
			145					150					155		
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr
		160					165					170			
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val
	175					180					185				
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn
190					195					200					205
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro
				210					215					220	
Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu
			225					230					235		
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp
		240					245					250			
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
	255					260					265				
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly
270					275					280					285



<222> (1173)..(1290)

<220>

<221> intron

<222> (1621)..(1717)

<220>

<221> exon

<222> (23)..(736)

<220>

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<222> (1128)..(1172)

<220>

<221> exon

<222> (1291)..(1620)

<220>

<221> exon

<222> (1718)..(2038)

<220>

<221> mat peptide

<222> (80)..(736)

<220>

<221> mat peptide

<222> (1128)..(1172)

<220>

<221> mat peptide

<222> (1291)..(1620)

<220>

<221> mat peptide

<222> (1718)..(2038)

<220>

<221> CDS

<222> (23)..(736)

<220>

<221> CDS

<222> (1128)..(1172)

<220>

<221> CDS

<222> (1291)..(1620)

<220>

<221> CDS

<222> (1718)..(2038)

&lt;400&gt; 146

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					Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu		
									-15					-10		
gta	gca	aca	gct	aca	ggt	gtc	cat	tct	cag	gtc	caa	ctg	gtg	cag	tct	100
Val	Ala	Thr	Ala	Thr	Gly	Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	
				-5				-1	1				5			
ggg	gct	gag	gtc	aag	aag	cct	ggg	gct	tca	gtg	aag	gtg	tcc	tgc	aag	148
Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	
		10					15					20				
gct	tct	ggc	tac	acc	ttc	acc	agc	tac	tgg	atg	cag	tgg	gta	cga	cag	196
Ala	Ser	Gly	Tyr	Thr	Phe	Thr	Ser	Tyr	Trp	Met	Gln	Trp	Val	Arg	Gln	
	25					30					35					
gcc	cct	gga	caa	gga	ctt	gag	tgg	atg	gga	gag	att	gat	cct	tct	gat	244
Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Glu	Ile	Asp	Pro	Ser	Asp	
	40				45					50					55	
agc	tat	act	aac	tac	aat	caa	aag	ttc	aag	ggc	aag	gcc	aca	ttg	act	292
Ser	Tyr	Thr	Asn	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	
			60						65					70		
gta	gac	aca	tcc	act	agc	aca	gcc	tac	atg	gag	ctc	agc	agc	ctg	aga	340
Val	Asp	Thr	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	
			75					80					85			
tct	gag	gac	acg	gcg	gtc	tat	tac	tgt	gca	aga	aat	agg	gac	tat	agt	388
Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Asn	Arg	Asp	Tyr	Ser	
		90					95					100				
aac	aac	tgg	tac	ttc	gat	gtc	tgg	ggc	caa	ggt	aca	ctg	gtc	acc	gtc	436
Asn	Asn	Trp	Tyr	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	
	105					110					115					
tcc	tca	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	484
Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
					125					130					135	
tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	532
Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
				140					145					150		
gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	580
Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
			155					160					165			
acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	628
Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
		170					175					180				
tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	676

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr  
 185 190 195  
 cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg 724  
 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val  
 200 205 210 215  
 gac aag aga gtt ggtgagagggc cagcacaggg agggaggggtg tctgctggaa 776  
 Asp Lys Arg Val  
 gccagggtca gcgctcctgc ctggacgcat cccggctatg cagtcccagt ccaggggcagc 836  
 aaggcaggcc ccgtctgcct cttcaccgag aggcctctgc ccgccccact catgctcagg 896  
 gagaggggtct tctggctttt tccccaggct ctgggcaggc acaggctagg tgccccctaac 956  
 ccaggccctg cacacaaagg ggcaggtgct gggctcagac ctgccaagag ccatatccgg 1016  
 gaggaccctg cccctgacct aagcccaccc caaaggccaa actctccact ccctcagctc 1076  
 ggacaccttc tctcctccca gattccagta actcccaatc ttctctctgc a gag ccc 1133  
 Glu Pro  
 220  
 aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca ggtaagccag 1182  
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
 225 230  
 cccaggcctc gccctccagc tcaaggcggg acagggtgcc tagagtagcc tgcattccagg 1242  
 gacaggcccc agccgggtgc tgacacgtcc acctccatct cttcctca gca cct gaa 1299  
 Ala Pro Glu  
 235  
 ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac 1347  
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 240 245 250  
 acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac 1395  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 255 260 265  
 gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc 1443  
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 270 275 280 285  
 gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac 1491  
 Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  
 290 295 300  
 agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg 1539  
 Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 305 310 315

ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca 1587  
 Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
 320 325 330

gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtgggggtgcg 1640  
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
 335 340

agggccacat ggacagaggc cggctcggcc caccctctgc cctgagagtg accgctgtac 1700

caacctctgt ccctaca ggg cag ccc cga gaa cca cag gtg tac acc ctg 1750  
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu  
 345 350 355

ccc cca tcc cgg gag gag atg acc aag aac cag gtc agc ctg acc tgc 1798  
 Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys  
 360 365 370

ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc 1846  
 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser  
 375 380 385

aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac 1894  
 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp  
 390 395 400

tcc gac ggc tcc ttc ttc ctc tat agc aag ctc acc gtg gac aag agc 1942  
 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
 405 410 415

agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct 1990  
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala  
 420 425 430 435

ctg cac aac cac tac acg cag aag agc ctc tcc ctg tcc ccg ggt aaa 2038  
 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 440 445 450

tgagtgcgac ggccggcaag ccccgctccc gaatt 2073

&lt;210&gt; 147

&lt;211&gt; 470

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

 <223> Description of Artificial Sequence: Designed heavy  
 chain of humanized anti-Fas antibody

&lt;400&gt; 147

 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
 -15 -10 -5



Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
           -1   1                          5                          10  
 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
       15                          20                          25  
 Thr Ser Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
   30                          35                          40                          45  
 Glu Trp Met Gly Glu Ile Asp Pro Ser Asp Ser Tyr Thr Asn Tyr Asn  
                           50                          55                          60  
 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Ser  
                           65                          70                          75  
 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
           80                          85                          90  
 Tyr Tyr Cys Ala Arg Asn Arg Asp Tyr Ser Asn Asn Trp Tyr Phe Asp  
       95                          100                          105  
 Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
  110                          115                          120                          125  
 Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
                           130                          135                          140  
 Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
                           145                          150                          155  
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
       160                          165                          170  
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
       175                          180                          185  
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn  
  190                          195                          200                          205  
 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro  
                           210                          215                          220  
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu  
                           225                          230                          235  
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
       240                          245                          250  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
       255                          260                          265  
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
       270                          275                          280                          285

<220>

<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the heavy chain  
of a humanized anti-Fas antibody

<400> 149  
agtgggtaaa acaggcccct ggacagggac ttgagtggat

40

<210> 150  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the heavy chain  
of a humanized anti-Fas antibody

<400> 150  
atccactcaa gtccctgtcc aggggcctgt tttaccact

40

<210> 151  
<211> 64  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the heavy chain  
of a humanized anti-Fas antibody

<400> 151  
aagaccgatg ggcccttggt ggaggctgag gagacgggtga ccagtgtacc ttggccccag 60  
acat

64

<210> 152  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the heavy chain  
of a humanized anti-Fas antibody

<400> 152  
gttcaagggc aaggccacaa taactgtaga cacatccgc

39

<210> 153  
<211> 39

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the heavy chain  
of a humanized anti-Fas antibody

<400> 153  
gcggatgtgt ctacagttat tgtggccttg cccttgaac

39

<210> 154  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the heavy chain  
of a humanized anti-Fas antibody

<400> 154  
agtgggtacg acaggcccct ggacaaggac ttgagtggat

40

<210> 155  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer to  
amplify a fragment of DNA encoding the heavy chain  
of a humanized anti-Fas antibody

<400> 155  
atccactcaa gtccttgtcc aggggcctgt cgtacccact

40

<210> 156  
<211> 2077  
<212> DNA  
<213> Artificial Sequence

<220>  
<221> sig peptide  
<222> (27)..(83)

<220>  
<221> intron  
<222> (741)..(1131)

<220>

<221> intron  
<222> (1177)..(1294)

<220>  
<221> intron  
<222> (1625)..(1725)

<220>  
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<222> (27)..(740)

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<222> (1132)..(1176)

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<222> (1295)..(1624)

<220>  
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<222> (1722)..(2042)

<220>  
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<222> (84)..(740)

<220>  
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<222> (1132)..(1176)

<220>  
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<222> (1295)..(1624)

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<222> (1722)..(2042)

<220>  
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<222> (27)..(740)

<220>  
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<222> (1132)..(1176)

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<222> (1295)..(1624)

<220>  
<221> CDS  
<222> (1722)..(2042)

&lt;220&gt;

<223> Description of Artificial Sequence: Designed DNA  
encoding the heavy chain of humanized anti-Fas  
antibody

&lt;400&gt; 156

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gggcgaaagc ttggcttgac ctcacc atg gga tgg agc tgt atc atc ctc ttc 53
                        Met Gly Trp Ser Cys Ile Ile Leu Phe
                        -15

ttg gta gca aca gct aca ggt gtc cac tct cag gtc caa ctg gtg cag 101
Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Val Gln Leu Val Gln
-10                        -5                        -1      1                        5

tct ggg gct gag gtc aag aag cct ggg gct tca gtg aag gtg tcc tgc 149
Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys
                        10                        15                        20

aag gct tct ggc tac acc ttc acc agc tac tgg atg cag tgg gta cga 197
Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Trp Met Gln Trp Val Arg
                        25                        30                        35

cag gcc cct gga cag ggc ctt gag tgg atg gga gag att gat cct tct 245
Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Glu Ile Asp Pro Ser
                        40                        45                        50

gat agc tat act aac tac aat caa aag ttc aag ggc cgg gtc aca atc 293
Asp Ser Tyr Thr Asn Tyr Asn Gln Lys Phe Lys Gly Arg Val Thr Ile
55                        60                        65                        70

act cga gac aca tcc act agc aca gcc tac atg gag ctc agc agc ctg 341
Thr Arg Asp Thr Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu
                        75                        80                        85

aga tct gag gac acg gcg gtc tat tac tgt gca aga aat agg gac tat 389
Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Arg Asp Tyr
                        90                        95                        100

agt aac aac tgg tac ttc gat gtc tgg ggc gaa ggg acc ctg gtc acc 437
Ser Asn Asn Trp Tyr Phe Asp Val Trp Gly Glu Gly Thr Leu Val Thr
105                        110                        115

gtc tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc 485
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
120                        125                        130

tcc tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc 533
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
135                        140                        145                        150

aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc 581
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
                        155                        160                        165

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ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga 629  
 Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly  
 170 175 180

ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc 677  
 Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly  
 185 190 195

acc cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag 725  
 Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys  
 200 205 210

gtg gac aag aga gtt ggtgagagggc cagcacaggg agggaggggtg tctgctggaa 780  
 Val Asp Lys Arg Val  
 215

gccaggctca gcgctcctgc ctggacgcat cccggctatg cagtcccagt ccagggcagc 840

aaggcaggcc ccgtctgcct cttcaccogg aggcctctgc ccgccccact catgctcagg 900

gagaggggtct tctggctttt tccccaggct ctgggcaggc acaggctagg tgcccctaac 960

ccaggccctg cacacaaagg ggcagggtgct gggctcagac ctgccaagag ccatatccgg 1020

gaggaccctg cccctgacct aagcccaccc caaaggccaa actctccact ccctcagctc 1080

ggacaccttc tctcctccca gattccagta actcccaatc ttctctctgc a gag ccc 1137  
 Glu Pro  
 220

aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca ggtaagccag 1186  
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro  
 225 230

cccaggcctc gccctccagc tcaaggcggg acagggtgcc tagagtagcc tgcattccagg 1246

gacaggcccc agccgggtgc tgacacgtcc acctccatct ctctctca gca cct gaa 1303  
 Ala Pro Glu  
 235

ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac 1351  
 Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp  
 240 245 250

acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac 1399  
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 255 260 265

gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc 1447  
 Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 270 275 280 285

gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac 1495

Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn		
				290					295					300			
agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	1543	
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp		
			305					310					315				
ctg	aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	1591	
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro		
		320					325					330					
gcc	ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggtgggaccc	gtgggggtgcg	1644				
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys							
	335					340											
agggccacat	ggacagagggc	cggtctcggcc	caccctctgc	cctgagagtg	accgctgtac	1704											
caacctctgt	ccctaca	ggg	cag	ccc	cga	gaa	cca	cag	gtg	tac	acc	ctg	1754				
		Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu					
		345					350					355					
ccc	cca	tcc	cgg	gag	gag	atg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	1802	
Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys		
				360					365					370			
ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	gtg	gag	tgg	gag	agc	1850	
Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser		
			375					380					385				
aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	cct	ccc	gtg	ctg	gac	1898	
Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp		
		390					395					400					
tcc	gac	ggc	tcc	ttc	ttc	ctc	tat	agc	aag	ctc	acc	gtg	gac	aag	agc	1946	
Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser		
	405					410					415						
agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	1994	
Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala		
	420				425					430					435		
ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tcc	ccg	ggt	aaa	2042	
Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys		
				440					445					450			
tgagtgcgac	ggccggcaag	ccccgctccc	gaatt	2077													

&lt;210&gt; 157

&lt;211&gt; 470

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;



<223> Description of Artificial Sequence: Designed  
heavy chain of humanized anti-Fas antibody

<400> 157

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
				-15					-10						-5	
Val	His	Ser	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
		-1	1				5					10				
Pro	Gly	Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	
	15					20					25					
Thr	Ser	Tyr	Trp	Met	Gln	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
	30				35					40					45	
Glu	Trp	Met	Gly	Glu	Ile	Asp	Pro	Ser	Asp	Ser	Tyr	Thr	Asn	Tyr	Asn	
				50					55					60		
Gln	Lys	Phe	Lys	Gly	Arg	Val	Thr	Ile	Thr	Arg	Asp	Thr	Ser	Thr	Ser	
			65					70					75			
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
		80					85					90				
Tyr	Tyr	Cys	Ala	Arg	Asn	Arg	Asp	Tyr	Ser	Asn	Asn	Trp	Tyr	Phe	Asp	
	95					100					105					
Val	Trp	Gly	Glu	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	
	110				115					120					125	
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	
				130					135					140		
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	
			145					150					155			
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	
		160					165					170				
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	
	175					180					185					
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	
	190				195					200				205		
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	
				210					215					220		
Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	
			225					230					235			
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	
		240					245					250				

345

345

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp  
 255 260 265

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
 270 275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn  
 290 295 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp  
 305 310 315

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro  
 320 325 330

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu  
 335 340 345

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn  
 350 355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile  
 370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr  
 385 390 395

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
 400 405 410

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys  
 415 420 425

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu  
 430 435 440 445

Ser Leu Ser Pro Gly Lys  
 450

<210> 158

<211> 29

<212> DNA -

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of DNA encoding the heavy chain  
 of humanized anti-Fas antibody

<400> 158

gatgcagtgg gtacgacagg cccctggac

29

346

<210> 159  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of DNA encoding the heavy chain  
 of humanized anti-Fas antibody

<400> 159  
 gtccaggggc ctgtcgtacc cactgcatc

29

<210> 160  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of DNA encoding the heavy chain  
 of humanized anti-Fas antibody

<400> 160  
 caagggccgg gtcacaatca ctcgagacac atc

33

<210> 161  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: PCR primer to  
 amplify a fragment of DNA encoding the heavy chain  
 of humanized anti-Fas antibody

<400> 161  
 gatgtgtctc gagtgattgt gacccggccc ttg

33

<210> 162  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Sequencing  
 primer for a DNA encoding the heavy chain of  
 humanized anti-Fas antibody

<400> 162

ctacaatcaa aagttcaagg

20

<210> 163  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Sequencing  
 primer for a DNA encoding the heavy chain of  
 humanized anti-Fas antibody

<400> 163  
 gactatagta acaactggta c

21

<210> 164  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Sequencing  
 primer for a DNA encoding the heavy chain of  
 humanized anti-Fas antibody

<400> 164  
 gtaccagttg ttactatagt c

21

<210> 165  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Sequencing  
 primer for a DNA encoding the heavy chain of  
 humanized anti-Fas antibody

<400> 165  
 gcagcccagg gccgctgtgc

20